

METHODS FOR IDENTIFYING SUITABLE NUCLEIC ACID NORMALIZATION PROBE SEQUENCES FOR USE IN NUCLEIC ACID ARRAYS

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ABSTRACT OF THE DISCLOSURE

Methods of identifying a sequence of a probe, e.g., a biopolymeric probe, such as a nucleic acid, that is suitable for use as a surface immobilized normalization probe on a nucleic acid array are provided. A feature of the subject methods is that a set of computationally determined initial candidate sequences are empirically evaluated to obtain functional data that is then employed to evaluate the candidate sequences for suitability as normalization probes. Sequences identified as suitable for use as normalization probes according to the subject methods are ones that do not cluster with other probes of the candidate set, exhibit high signal intensity and exhibit substantially no differential expression across a large number of samples. The subject invention also includes algorithms for performing the subject methods recorded on a computer readable medium, as well as computational analysis systems that include the same. Also provided are nucleic acid arrays produced with probes having sequences identified by the subject methods, as well as methods for using the same.